

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 21, 1999, 01:52:19 ; Search time 16.06 Seconds

(without alignment) 1283.756 Million cell updates/sec

Title: US-09-126-945-2

Perfect score: 1785

Sequence: 1 MGSASPGSLSSVSPHLLP.....GITKPDISQRLVQVHP1 335

Scoring table: BLOSUM62

Searched: 201082 seqs, 61543640 residues

Database :
1: SP:Archaea:*
2: SP:Bacteria:*
3: SP:Fungi:*
4: SP:Invertebrate:*
5: SP:Mammal:*
6: SP:Plant:*
7: SP:Phage:*
8: SP:Organelle:*
9: SP:Protist:*
10: SP:Rodent:*
11: SP:Vertebrate:*
12: SP:Virus:*
13: SP:Unclassified:*
14: SP:Unclassified:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1785	100.0	335	4	095238 homo sapien
2	487.5	27.3	363	5	097145 strongyloce
3	417	23.4	532	5	019695 caenorhabd
4	299	16.8	255	4	095175 homo sapien
5	288	16.1	253	11	092266 mus muscu
6	283	15.9	336	6	062804 ovis arie
7	274	15.4	432	13	093425 columba co
8	263.7	14.3	581	13	097125 streptococ
9	257.5	14.0	581	13	097125 streptococ
10	256.5	14.4	300	11	070223 homo sapien
11	255.5	14.3	440	13	097057 caenorhabd
12	252.5	14.1	481	5	017057 caenorhabd
13	249.5	14.0	385	4	014319 homo sapien
14	249	13.9	348	4	099718 homo sapien
15	245	13.7	663	4	099607 homo sapien
16	245	13.7	663	4	060435 homo sapien
17	245	13.7	663	4	060435 homo sapien
18	242	13.6	426	6	082803 ovis arie
19	242	13.6	426	6	082803 ovis arie
20	241	13.5	533	4	015724 homo sapien
21	239	13.4	471	13	057556 caenorhabd
22	238.5	13.4	471	13	057556 caenorhabd
23	235.5	13.2	371	11	035275 homo sapien
24	230.5	12.9	490	13	097057 caenorhabd
25	229	12.8	490	13	097057 caenorhabd
26	225	12.5	390	13	095849 homo sapien
27	224	12.5	390	13	095849 homo sapien
28	224	12.5	390	13	095849 homo sapien
29	219	12.3	454	4	075849 homo sapien

ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT:	335 AA.
095238	095238			
1D	095238			
AD	095238:			
DY	01-MAY-1999 (17EMBLrel. 10, Created)			
DY	01-MAY-1999 (17EMBLrel. 10, Last sequence update)			
DY	01-MAY-1999 (17EMBLrel. 10, Last annotation update)			
DE	ETS TRANSCRIPTION FACTOR PDEF.			
DT	PDEF.			
GN	PDEF.			
OC	Eukaryota; Metazoa; Chordata; Vertebrate; Mammalia;			
OC	Eutheria; Placental; Carnivora; Hominoidea; Homo.			
NC	[1]			
NP	SEQUENCE FROM N.A.			
RC	TISSUE=PROSTATE;			
RA	OETGEN P., FINER E., ABAHALI Y., THANHONGSAK U., DUBE A.,			
RA	BOLTAJ J., BROWN L., KUNSC H., LIEBMANN T.A.;			
RT	Isolation and characterization of a novel prostate			
RT	epithelium-specific Ets transcription factor, PDEF. *			
RL	Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.			
RL	EMBL: AF071538; AAC95286.1; -			
SO	SEQUENCE 335 AA: 37517 MW: 8745D88 CRC32:			
Query Match	100.0%:	Score 1785:	DB 4:	Length 335:
Best Local	Similarity 100.0%:	Pident No 94:	4e-133:	
Matches 335:	Conservative 0:	Mismatches 0:	Indels 0:	Gaps 0:
0Y	1	MKSAAPRLSSVYSHELLPDTVYRFTGLKKAAGANGLERRQMSPPATPEGLSAYFL 60		
Db	1	MKSAAPRLSSVYSHELLPDTVYRFTGLKKAAGANGLERRQMSPPATPEGLSAYFL 60		
0Y	61	STFAMLYPPEDSNAKAPGASRKEPEEPEDCPYIDSOAPAGSLDVGGLTLPEHSLE 120		
Db	61	STFAMLYPPEDSNAKAPGASRKEPEEPEDCPYIDSOAPAGSLDVGGLTLPEHSLE 120		
0Y	121	OVQSNVGVGLKIDIEACKLMLITADMDKMSFSNVOKMLMLTIEQYRLDPYKGAFOELAG 180		
Db	121	OVQSNVGVGLKIDIEACKLMLITADMDKMSFSNVOKMLMLTIEQYRLDPYKGAFOELAG 180		
0Y	181	KELCANESEORRORPRLAGGVYAHMLDIKKAAMKERTSGALIKCSSESPTDSY 240		
Db	181	KELCANESEORRORPRLAGGVYAHMLDIKKAAMKERTSPALIKVCASTSESPTDSY 240		
0Y	241	DSSCSGPIHLMQFLKELLKPHSGYFRMLKENGIFPTEDSQVAYLMLNGIRKRPAM 300		
Db	241	DSSCSGPIHLMQFLKELLKPHSGYFRMLKENGIFPTEDSQVAYLMLNGIRKRPAM 300		
0Y	301	NTDKLSRSIRYTKKGIIRKRPDISORLYVQGVPI 335		
Db	301	NTDKLSRSIRYTKKGIIRKRPDISORLYVQGVPI 335		

RA BONFIELD J., BURTON J., CONNELL M., CORSEY T., COOPER J., COULSON A.,
 RA BRAYTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
 RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIE M., JOHNSTON L.,
 RA JONES M., KERSEBAUM J., KINGSTON J., LAISTER N., LATHEILLE P.,
 RA JONES M., JENKINS J., KIRBY C., KIRKPATRICK A., MORTIMER B., O'CALLAGHAN M.,
 RA PALSON N., PERCY C., RICHARDS A., ROBERTSON A., SANDERSON D., SHONKKEIN R.,
 RA SALDON N., SMITH A., SONNENWALD E., STADEN S., SUTHERLAND J., WOODMAN R.,
 RA THIERREY-MIES J., THOMAS K., VANDIN M., VANDEKAMP K., WATSON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPRATT J., WOLFEHAN P.,
 RT 2.2 Mb of contiguous nucleotide sequence from chromosome III of *C.
 elegans*.
 RL Mature 368:32-38(1994).
 RL 12
 RP SEQUENCE FROM N.A.
 RA HALLSMORTH K.;
 RL Submitted (DEC-1995) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA WATERSTON R.;
 RL Submitted (NOV-1995) to the EMBL/Genbank/DBJ databases.
 RL PRN1: AF0517; AF0518; AF0519; AF0520; AF0521; AF0522; AF0523; AF0524;
 DR PRN1: AF0517; AF0518; AF0519; AF0520; AF0521; AF0522; AF0523; AF0524;
 SO SEQUENCE 532 kb; 60199 bp; 98067676 CIRC32;

[illegible]

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DE E74-LIKE FACTOR 5.
GN ELF5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Placental; Catarrhini; Hominoidea; Homo.
RN [1] JENSEN FROM N.A.
RA ZHOU J., NG A.I.N., TYMS M.J., JERMIN L.S., SEH A.K., THOMAS R.S.,
RA KOHL I., NG A.I.N., TYMS M.J., JERMIN L.S., SEH A.K., THOMAS R.S.,
RT "A novel transcription factor, ELF5, belongs to the ELF subfamily of
RT ETS genes and maps to human chromosome 11p13-15, a region subject to
RT LOH and rearrangement in human carcinoma cell lines."
RL Oncogene 17:0-0(1998).
DR EMBL: AF049703; AAC79755.1;
SQ SEQUENCE 255 AA: 30121 MW: 51579A0D CRC32:

Query Match 16.8% Score 399, DB 4: Length 255:
Best Local Similarity 33.2% Pred. No. 2,38-19:
Matches 70: Conservative 42: Mismatches 79: Indels 20: Gaps 4:

OY 135 ETACKLNTADPMDSPSVOKMLTWHQYRIPLPKAKF--QELAGRELCANSEDFR 192
DB 39 QTRADSYTSHPEVTRKRWHEMLQCCDDQKRLQNCISFCNFISGLQCLSTDEEY 98
OY 193 QNSPLGQDVLAHL-----DIKSAKANKERTSPKATNYCASTSESTDEY 240
DB 99 EAVAGCEYLFLFLOHNTQCYSPFNDAEENKATIDYASN---CLMTSGIKSDCHS 154
OY 241 DSCSGCPHLMQFLKELLKPHSYGFRLNENRGFIETDSQVAYLNGIKRNPAM 300
DB 135 HSRITSLOSSHLMFVADLLSPENCGILEMEDEGCFRNVKSPALATKMGKRNDRM 214
OY 301 MTKLRSIRQYTKGIRKRPDISQRLYQF 331
DB 215 TTKLSRLAKTYIKTGILENDV--RLVLYNF 243

RESULT 5
O922K6 PRELIMINARY: PRT: 253 AA.
AC Q922K6:
DT 01-MAY-1999 (TRENDArel. 10, Created)
DT 01-MAY-1999 (TRENDArel. 10, Last sequence update)
DE E74-LIKE FACTOR 5.
GN ELF5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RA SEQUENCE FROM N.A.
RA ZHOU J., NG A.I.N., TYMS M.J., JERMIN L.S., SEH A.K., THOMAS R.S.,
RT "A novel transcription factor, ELF5, belongs to the ELF subfamily of
RT ETS genes and maps to human chromosome 11p13-15, a region subject to
RT LOH and rearrangement in human carcinoma cell lines."
RL Oncogene 17:0-0(1998).
DR EMBL: AF049703; AAC79755.1;
SQ SEQUENCE 253 AA: 29971 MW: 7862A0B4 CRC32:

Query Match 16.1% Score 288, DB 11: Length 253:
Best Local Similarity 33.9% Pred. No. 2,28-18:
Matches 68: Conservative 43: Mismatches 82: Indels 14: Gaps 5:

OY 135 ETACKLNTADPMDSPSVOKMLTWHQYRIPLPKAKF--QELAGRELCANSEDFR 192
DB 39 QTRADSYTSHPEVTRKRWHEMLQCCDDQKRLQNCISFCNFISGLQCLSTDEEY 98
OY 193 QNSPLGQDVLAHL-----DIKSAKANKERTSPKATNYCASTSESTDEY 240
DB 99 EAVAGCEYLFLFLOHNTQCYSPFNDAEENKATIDYASN---CLMTSGIKSDCHS 154
OY 301 MTKLRSIRQYTKGIRKRPDISQRLYQF 331
DB 215 TTKLSRLAKTYIKTGILENDV--RLVLYNF 243

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OY 245 SCQPIHLMQFLKELLKPHSYGFRLNENRGFIETDSQVAYLNGIKRNPAMNDK 304
DB 157 SIQSSHLMFVRODLLSPENCGILEMEDEGCFRNVKSPALATKMGKRNDRYK 216
OY 305 LRSIRQYTKGIRKRPDISQRLYQF 331
DB 217 LRSRLAKTYIKTGILENDV--RLVLYNF 241

RESULT 6
O62804 PRELIMINARY: PRT: 336 AA.
AC O62804:
DT 01-AUG-1998 (TRENDArel. 07, Created)
DT 01-AUG-1998 (TRENDArel. 07, Last sequence update)
DE TRANSCRIPTION FACTOR GABP ALPHA SUBUNIT (PROMOTER).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
RN [1]
RA SEQUENCE FROM N.A.
RA EKHART T., EATY R.D., OSTROMSKI M.C., ROBERTS R.M.;
RA EKHART T., EATY R.D., OSTROMSKI M.C., ROBERTS R.M.;
DR EMBL: AF051717; AAC39262.1;
DR PFAM: PF00178; Ets: 1.2021.1;
DR PROSITE: PS00345; ETS_DOMAIN_1: 1.
DR PROSITE: PS00346; ETS_DOMAIN_2: 1.
FT NON_TER 1 1
SQ SEQUENCE 336 AA: 38033 MW: 8CFE931F CRC32:

Query Match 15.9% Score 283, DB 6: Length 336:
Best Local Similarity 32.2% Pred. No. 9,28-15:
Matches 84: Conservative 43: Mismatches 115: Indels 46: Gaps 9:

OY 78 PGASSREPPPEPEPCPYIDQAPAGSLDPGGLTLEBHSLEQVOSVNGEVLKDIET 137
DB 8 PDHNAHEALVLEAHYI-----TLDGKAIITTSIDETSEQYTRMAA--ALGVRKE 58
OY 138 CCLNTADPMDSPSVOKMLTWHQYRIPLPKAKF--QELAGRELCANSEDFRSPU 197
DB 59 QERGLDITDPLQNSDYLRKRWHEMLQCCDDQKRLQNCISFCNFISGLQCLSTDEEY 98
OY 198 GQDVLAHLMDIKMSAANKER-----TSPAIHVCSTSESN 235
DB 118 REELTMSHLETKRYLASOEHNEIYIDQVQIIPASVQSPALKAINKSSKAK 177
OY 236 TD-----SEVSSCSQ-----PIHLMQFLKELLKPHSYGFRLNENRGFIETDS 284
DB 178 VQRAPISEDRSPKNTGNGQIQLOMQLFELLDKNDK--CLSNVQDE--GERFLNQP 235
OY 285 AVAYALMGIRKRNPNANDLERSIRQYTKGIRKRPDISQRLYQF 332
DB 236 ELVAGKQWRKRNPNMYERLSRLAKTYIKTGILENDV--RLVLYNF 241
OY 236 ELVAGKQWRKRNPNMYERLSRLAKTYIKTGILENDV--RLVLYNF 241

RESULT 7
O93435 PRELIMINARY: PRT: 432 AA.
AC O93435:
DT 01-NOV-1998 (TRENDArel. 08, Created)
DT 01-NOV-1998 (TRENDArel. 08, Last sequence update)
DE FIL TRANSCRIPTION FACTOR.
GN FIL.
OS Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianidae; Coturnix.
RN [1]
RA SEQUENCE FROM N.A.

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RX MEDLINE; 98358003.
 RA MAGER A.M., GRAPIN-BOTTON A., LADJALI K., MEYER D., WOLFF C.M.,
 RT STEIGLER P., BONNIN M.A., Remy P.:
 The avian *lil* gene is specifically expressed during embryogenesis in
 the mesoderm of neural crest cells giving rise to mesenchyme.
 DR EMBL: Y14773; CAAT5078.1; -.
 DR EMBL: Y14774; CAAT5078.1; -.
 DR PFAM: PF00178; Ets.1.
 DR PROSITE: PS00345; ETS_DOMAIN.1; 1.
 DR PROSITE: PS00346; ETS_DOMAIN.2; 1.
 SO SEQUENCE 433 AA; 48761 MW; 8F0117BD CRC32:

Query Match 15.4%; Score 274; DB 13; Length 432;
 Best Local Similarity 34.8%; Pred. No. 8 3e-12;
 Matches 77; Conservative 31; Mismatches 75; Indels 38; Gaps 9;

QY 143 ITADNDSPSPVOKMLTETHOYRLPBGKA-FOELAGELCAASDEOF-ROKSPGLGD 200
 DB 126 VPADPTLMTQEHVHOLEMAKEVGLIDETFFOMDGEKLCNNKDDFLRTTSLYTE 185
 QY 201 VHAHDIKRSAMKERTSPKINCA-----TSESR----- 236
 DB 166 VILSHLSYRESSLLAVNTPS--HTPSSRLAKESGPPAAGNWKMTIDCQRPPT 243
 QY 236 -----TDSEVSSCSGCPHLMQFLKELLPHSYGRFIRMLNKKKFKIEDSAQVAR 290
 DB 244 QILGFTSSRLANPSGO-IDLQFLFL-LLSDSSNCSITW-EGTNGEKMTDPDEVAR 300
 QY 291 WGRNRPANMYDKLSRSTQYKKKGIKKPDISQRLVOP 331
 DB 301 MGRKSPMNMYDKLSRLATYYDKMLNKNVH-GKRYLYNF 340
 RESULT 8
 QY 09YH25 PRELIMINARY; PRT: 435 AA.
 ID Q15723
 DC 01-MAY-1995 (TREMBL) 10. Created
 DT 01-MAY-1995 (TREMBL) 10. Last sequence update
 DT 01-MAY-1999 (TREMBL) 10. Last annotation update
 DE E74-LIKE FACTOR-1.
 GN ZEP1.
 OS Brachydanio rerio (zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Actinopterygii; Neopterygii;
 OC Cyprinidae; Cypriniformes; Cyprinidae; Cyprinidae.
 OC Cyprinidae; Cyprinidae; Danio.
 RN [1] J. Inoué, K. Sato, Danio.
 RP SEQUENCE FROM N.A.
 RC TISSUE-KIDNEY.
 RA UCHIDA H., ZON L., MIYAZAKI Y., NIMER S.;
 RT Zebrafish (Danio rerio) to the EMBL/Genbank/DBJ databases.
 DR EMBL: U84615; RAD0475.1; -.
 DR PROSITE: PS00345; ETS_DOMAIN.1; 1.
 DR PROSITE: PS00346; ETS_DOMAIN.2; 1.
 SO SEQUENCE 435 AA; 48339 MW; ECGPCFD4 CRC32:

Query Match 14.9%; Score 265.5; DB 13; Length 435;
 Best Local Similarity 30.1%; Pred. No. 4.9e-16;
 Matches 86; Conservative 47; Mismatches 91; Indels 57; Gaps 12;
 QY 88 EEPQCP-VIDSOAPGSDLVPGGLLEHS-----LEQVSNV-----VGRV----- 131
 DB 26 DDPSEFPAIVEYQPADLMQVYSGDELGTNGJMDADQOYVEENMDGVLSETPV 85
 QY 131 -----LDIFPACLLINTADPMWSPNV--QKMLTETHOYRLPBGKAFOELAGKE 182
 DB 86 SGGDWKEITDAEALLAME-----SRNLDKRNKIRH-----TGNILETD 127

QY 183 LCAMSEDFROKSPGLGDVH-----AHD-----TKRSAMKERTSPAHVCASTSE 232
 DB 128 LEYSILRP--EHSNGDVADHDTSSLEDEYPRKRSKPRKTRV--KRPAPCSPTIN 184
 QY 233 ESMTDESEVSSCSGCPHLMQFLKELLKPHSYGRFIRMLNKKKFKIEDSAQVAR 292
 DB 185 FPLPLKRSKSGGWTLYMEFLALLDDKRTOPCYIKTQREGRIFRLVDSKAVSLNG 244
 QY 293 IKRNPANMYDKLSRSTQYKKKGIKKPDISQRLVOP 331
 DB 245 KKKKPDNMYETMGALATYYDKMLNKNVH-GKRYLYNF 340

RESULT 9
 ID Q15723
 DC 01-MAY-1995 (TREMBL) 01. Created
 DT 01-MAY-1995 (TREMBL) 01. Last sequence update
 DT 01-MAY-1999 (TREMBL) 10. Last annotation update
 DE ETS TRANSCRIPTION FACTOR.
 GN NERF-2.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homidae; Homo.
 RN [1] J. Inoué, K. Sato, Danio.
 RP SEQUENCE FROM N.A.
 RC TISSUE-SPLEEN, FETAL LIVER, FETAL BRAIN.
 RA OETGEN P., AKABALI Y., BOLTAJ J., BEST J., KUNSCH C.,
 RA LIBERMAN T.A.;
 RT Characterization of NERF, a novel transcription factor related to
 the Ets factor ELF-1.
 DR EMBL: G11810; J01672091-5106(1995).
 DR PROSITE: PS00345; ETS_DOMAIN.1; 1.
 DR PROSITE: PS00346; ETS_DOMAIN.2; 1.
 SO SEQUENCE 581 AA; 62711 MW; 2EE2228A CRC32:

Query Match 14.4%; Score 257; DB 4; Length 581;
 Best Local Similarity 25.5%; Pred. No. 4.2e-15;
 Matches 77; Conservative 50; Mismatches 97; Indels 78; Gaps 9;

QY 43 FSPAPRPGGLSAFLSYFDMLY-PEDSMAKAPGASREPEEPCQPVDS----- 99
 DB 39 FVPSARLEQGYADQVLYVDDEYMDQVA-----EEQVETENETVEASVHS 87
 QY 99 -----QAPASDLVPGGLTLEHSLEQVSNVGEVLYDLTACKLLNTADPMD 149
 DB 88 NACDRTIRAEALHMSPTLQDSSTEFIRHANNPDI--ETIVYVSTESSEPM 145
 QY 150 WSSNVQMLMTTHOYRLPBGKAFOELAGELCAASDEOFROKSPGLGDVLAHMD 209
 DB 146 TSP-----IPSDSHEHMKKK--VGRKKTQOSPISNG----- 179
 QY 210 KSNAMKERTSPGALHCASTSESMTDSVSSCSGCPHLMQFLKELLKPHSYGRF 269
 DB 179 SPGLKIRKPRG-----KGTTLTLEHLLDCKRTOPCY 216
 QY 270 FWMENKGIKIEDSAQVARLMGIRKRPANMYDKLSRSTQYKKKGIKKPDISQRLV 329
 DB 217 KTWQREKIFKLYDSKAVSKLMKHKRKNPDNMYETMGALATYYDKMLNKNVH-GKRYLYNF 244
 QY 330 OF 331
 DB 276 OF 277
 RESULT 10
 ID Q10273 PRELIMINARY; PRT: 300 AA.
 DC 07-07-93

AC 070273:
 DT 01-AUG-1998 (TREMblrel. 07, Created)
 DT 01-AUG-1998 (TREMblrel. 07, Last sequence update)
 DT 01-MAY-1999 (TREMblrel. 10, Last annotation update)
 DE ETS HOMOLOGOUS FACTOR (EHF) (EHF).
 GN EHF.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 CC Eukaryota; Mollusca; Scutigerma; Mollusca; Mollusca; Mollusca;
 RP SEQUENCE FROM N.A.
 RC TISSUE-PITUITARY;
 RX MEDLINE: 98262938.
 RA BOCHERT M.A., KLEINBAUM L.A., SUN L.Y., BURTON F.H.;
 RT "Molecular cloning and expression of Ehf, a new member of the ets
 RT transcription factor/oncogene gene family";
 RL Blochm. Biophys. Res. Commun. 246:176-181(1998).
 DR EMBL: AF033562; AF04119.1; .
 DR EMBL: AF033562; AF04119.1; .
 DR PDB: 1P00178; Etf: 1.
 SO SEQUENCE 300 AA: 34903 MW: 383FE2B6 CRC32:
 Query Match 14.4% Score 256.5; DB 11: Length 300;
 Best Local Similarity 28.0%; Pred. No. 1.9e-15;
 Matches 69; Conservative 47; Mismatches 65; Indels 65; Gaps 9;
 Oy 167 PMDSNSNOKWILTEHOYRLPRYKAGT--LAGEELCANESEPPORSLGQDYLHA 204
 Db 47 POUTYKVOVEMQLHLDITNOLASCIPROFEDISGELASNSLOEFTPAAGSACOLLYS 106
 Oy 205 HL-----DIWNSA---ANMKERTSGAIIHCASISSESWT-----DSVDV--- 242
 Db 107 NLQHLKMNQCCSDLPQSAHNYVYKTDPSLN---TWKEENLIDPSTGVLDLDS 163
 Oy 242 -SSCSGQ-----P-----HMORTKELLPKSY 265
 Db 164 KTFCHQISMTTSHLPVASEPDMKREOHQVYKSHKTHMPDRTLWFERIDILSPKN 223
 Oy 266 GEFIRLMNKENGIFKIEDSAQVRLMGIKRNPRAMMYTKLSINIOYKGIKIPDISQ 325
 Db 224 PGLIKMEDRSGLIFRFLKSEAVNALQMKRNNSSYKRLSRAMRYVYRELIERVD-GR 282
 Oy 326 RLTVQF 331
 Db 283 RLTVQF 288
 RESULT 11
 09YH05 PRELIMINARY: PRT: 440 AA.
 AC 09YH05:
 DT 01-MAY-1998 (TREMblrel. 10, Created)
 DT 01-MAY-1998 (TREMblrel. 10, Last sequence update)
 DE TRANSCRIPTION FACTOR ERF1.
 DE TRANSCRIPTION FACTOR ERF1.
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Actinopterygii; Neopterygii;
 CC Teleostei; Euteleostei; Acanthopterygii; Perciformes;
 CC Tetraodoniformes; Tetraodonidae; Tetraodonidae; Fugu.
 GN [1]
 RP SEQUENCE FROM N.A.
 RA VILLARD L., TASSON F., CRNOCORAC-JURCEVIC T., CLANCY K.,
 RA GARDINER K.;
 RT "Analysis of pufferfish homologues of the A-T-rich human Atp gene";
 RL Gene 210:17-24(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA TASSON F., VILLARD L., CLANCY K., GARDINER K.;
 RT "Structure, sequence characteristics, and synteny relationships of
 RT the transcription factor ERF1, the splitting factor U2AF5 and the
 RT cytoplasmic beta-synthesase genes from Fugu rubripes";

RL Gene 226:211-223(1999).
 DR EMBL: AF090120; AAD3395.1;
 SO SEQUENCE 440 AA: 49595 MW: 0E3E74F6 CRC32:
 Query Match 14.3% Score 255.5; DB 13: Length 440;
 Best Local Similarity 24.6%; Pred. No. 4e-15;
 Matches 78; Conservative 50; Mismatches 110; Indels 79; Gaps 8;
 Oy 60 LSYEDMLYEPSEMAAKAPGASSSEEPPEPECCVIDSO--APASQJLDPGCLLEH 117
 Db 107 LULIEYKVEVEVVIDPMAEGEALVEDGQLAVRSCGLSDPESQVTRMAALH 166
 Oy 118 SLEVOVSAYVEVLADIECTALNTADPMDSNSNOKWILTEHOYRLPRYKAGT 177
 Db 167 REEDVY-----LAIPIVPLASADQVYHMAVWVKEENIDEMIGSH 209
 Oy 178 LAGEELCANESEPPORSLGQDYLHMLDIKMSANMKERTSGAIIHCASISSESWT 237
 Db 210 IEGHDLSPGSEFQAKYF-NEIILSHLELAK-----YLAQDQSGSD 254
 Oy 238 SEV-----DSSCSGQ-----PRLMQF 255
 Db 235 AVYTIIDPQIIPYVTPAIKYLAKSGRAPRISGERSGNTGNGOIMQNF 314
 Oy 256 KELLKPHSIFRTIRLMKENGIFKIEDSAQVRLMGIKRNPRAMMYTKLSINIOYK 315
 Db 315 LELIDKKA--HDCIYRGESEFRLMQLVNMHQKRNKPTMYTILSRALRYTID 372
 Oy 316 GIKKPOLISORLYQFV 332
 Db 373 DMISKVO-GKRFVNFV 388
 RESULT 12
 017057 PRELIMINARY: PRT: 481 AA.
 AC 017057:
 DT 01-JAN-1998 (TREMblrel. 05, Created)
 DT 01-MAY-1998 (TREMblrel. 05, Last sequence update)
 DE C24A1.2 PROTEIN.
 GN C24A1.2
 OS Caenorhabditis elegans
 CC Eukaryota; Metazoa; Secernentea; Rhabditia; Rhabditia;
 CC Rhabditia; Rhabditidae; Rhabditidae; Pelodactylina; Caenorhabditis.
 GN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-BRISTOL N2;
 RX MEDLINE: 94150718.
 RA WILSON R., AINSWORTH R., ANDERSON K., BAYNES C., BERKS M.,
 RA BOWFIELD J., BURTON J., CONNELL N., COOPER J., COULSON A.,
 RA GARDINER K., GREEN S., DOWD J., DOWD J., DOWD J., DOWD J.,
 RA JONES M., KESHERV A., KESTEN J., LISTER N., LATREILLE P.,
 RA LIGHTNING J., LLOYD C., MCHURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIFKEN L., ROOPER A., SAUNDERS D., SHOWNKEEN R.,
 RA SHALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
 RA THREER-MILES J., THOMAS K., VAUDIN M., VAUGHAN K., WATSON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPOFFORD J., WOHLIDAN P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans";
 RL Nucleic Acids Res. 22:3683-3692(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA STRAIN-BRISTOL N2;
 RC CONNELL N.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA STRAIN-BRISTOL N2;
 RC WATSON R.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF024491. AAB70311.1. -
 DR PFM: P00178; Ets: 1.
 DR PROSITE: PS00345; ETS.DOMAIN.1: 1.
 DR PROSITE: PS00346; ETS.DOMAIN.2: 1.
 SO SEQUENCE 481 AA: 53773 MW: 575FAEB8 CRC32:

Query Match
 Best Local Similarity 14.1%; Score 252.5; DB 5; Length 481;
 Matches 45; Conservative 20; Mismatches 22; Indels 1; Gaps 1;
 Oy 246 GQHLNQLQFKEKLLKPHSGRGFRIMKNEKIKEDSQAQVRLMGIRKNRPMAYDKL 305
 Db 335 GQVLYLWFLRLLDODYSPTFKIKDQAKCIKLVDSKAVSLMGKMKPKPMYETM 394
 Oy 306 SSTIQQYKKKGIKEDSISQRLAYQYH 333
 Db 395 GRALRYQGIQKQVD-GQRLVYRFH 421

RESULT 13
 O14319 PRELIMINARY; PRT: 385 AA.
 AC O14319;
 DT 01-NOV-1996 (TREMURel. 01, Created)
 DT 01-NOV-1996 (TREMURel. 01, Last sequence update)
 DT 01-MAY-1999 (TREMURel. 10, Last annotation update)
 DE FTL-1.
 GN Homo sapiens (Human).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE: 93176799.
 RA KROMS R., MAY W., DENNY C., RASKIND W., MOORE J., MAKI R.A., BECK E.,
 RT "Human FTL-1 localises to chromosome 11q24 and has an aberrant
 RT transcript in neurocysticercosis";
 RL Blochlin. Biophys. Acta 1172:155-158(1993).
 DR EMBL: M93255; AAB58480.1. -
 DR PFM: P00178; Ets: 1.
 DR PROSITE: PS00345; ETS.DOMAIN.1: 1.
 DR PROSITE: PS00346; ETS.DOMAIN.2: 1.
 SO SEQUENCE 385 AA: 43433 MW: 0820C243 CRC32:

Query Match
 Best Local Similarity 14.0%; Score 249.5; DB 4; Length 385;
 Matches 87; Conservative 40; Mismatches 107; Indels 77; Gaps 12;
 Oy 79 GASSREPEPEPQCVISQAPAGSLDIVEGLT-----LEHSLDQVQSWVGEV 130
 Db 3 GGLAGRAEPIYDCV-----SKSKLVGGESNPKNINSYDKRNGPPNNNTTNE- 56
 Oy 131 LKDIETACKLINTADPMQSPSNQKMLMTEHGYLTPMKR-KROLAKGKICANSE- 189
 Db 56 -----RRIYVPADALIVTOEHQVLMELAIKSIEMIDTSFQNMOKKELCKANKE 107
 Oy 190 QFRGSRPL-GGDTLAHL-----DIMSAAKKE 217
 Db 108 DFLVATLLTNTETVLSLSTRESSLLAVNTSHTDSSRLSVKPEYDSVRGANGNN 167
 Oy 218 RTSP-----GAHYCASTSEE-----SRTQSEVSSGQGTILNQFKEKLL 260
 Db 168 NMSCLKKSPPLGGAGQOTISKNTPOPOPOVQIGTSPSLNAPSGQ-IDNQVTLLE-LL 225
 Oy 261 KPHSYGRIRMLKKEKIKEDSAQVAVRLMGIRKNRPMAYDKLSRSIQYKKGIIRK 326
 Db 226 SSSNASCMTL-EGTNEERMTDDEAVARNGQKRSKPNMNTKLSRLRKYTDKINIMTK 284
 Oy 321 PQLSKLYQGF 331

Db 285 VH-GKRYAKF 294

RESULT 14
 ID 099718 PRELIMINARY; PRT: 348 AA.
 AC 099718;
 DT 01-MAY-1997 (TREMURel. 03, Created)
 DT 01-MAY-1997 (TREMURel. 03, Last sequence update)
 DT 01-NOV-1996 (TREMURel. 08, Last annotation update)
 DE Eukaryotic-specific TRANSCRIPTION FACTOR ESS-1A.
 GN ESS-1.
 OS Homo sapiens (Human).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=ADIPOCYTE, PANCREATIC CARCINOMA;
 RX MEDLINE: 9373019.
 RA OETGEN P., ALANI R.M., BARGINSKI M.A., BRON L., ABRAMALI Y.,
 RA BOLTAN J., KUNSCHE C., WONGER K., LIBERMAN T.A.,
 RT "Isolation and characterization of a novel epithelium-specific
 RT transcription factor, ESS-1, a member of the ets family";
 RL Mol. Cell. Biol. 17:4419-4431(1997).
 DR EMBL: U73844; AAB55824.1. -
 DR PFM: P00178; Ets: 1.
 SO SEQUENCE 348 AA: 39357 MW: 274B3FA2 CRC32:

Query Match
 Best Local Similarity 13.9%; Score 249; DB 4; Length 348;
 Matches 89; Conservative 53; Mismatches 95; Indels 128; Gaps 16;
 Oy 55 LSAFYETPKYEDSSMAKAKPAGSSREPEPEPQCVISQAPAGSLDIVEGLT 114
 Db 7 ISNFSNFPANYSSEDTLASVPA-----ATFGDDLV--LTL 44
 Oy 115 E-EHSELYQV-SWVGEVLKDIETACKLINTADPMQSPSNQKMLM-TEHGYRLP 169
 Db 45 SNFQMSLDTGETAKSLGE-----OQFPMKSTQVLMISYQVKNKRYDAS 88
 Oy 170 PMKRFQELAKGICANSEPRF-QRSLQCVLAHL-DIKSKA-----AM- 216
 Db 89 AIFSCKDMGATLCKALIEELVFGPL-GQLQHQLRJUTSSSELSWILEKOG 117
 Oy 216 ---KERTSPGAHYCASTSESWTP-----SEVD----- 242
 Db 148 MARQDLPEPPDQGSFPAQELLDVSTAGTASRSSHSSDSGSDVDLDLPDGLKLFSD 207
 Oy 242 -SSCS-----GQF-----IHMQFKEKLLKPHSYG 267
 Db 208 GFDDKKGDPKRRGRKRPKRLSKETWOCLEKSKAPRGHLMETIRDLVHLE 267
 Oy 267 RFTMLKKEKIKEDSQAQVAVRLMGIRKNRPMAYDKLSRSIQYKKGIIRPDISOR 326
 Db 268 GLMKREHNGVFFLRSSAVALGQKKNKNYETKLSRLRKYTDKINIMTK-GRR 326
 Oy 327 LYTKF 331
 Db 327 LYTKF 331

RESULT 15
 ID 099607 PRELIMINARY; PRT: 663 AA.
 AC 099607;
 DT 01-MAY-1997 (TREMURel. 03, Created)
 DT 01-MAY-1997 (TREMURel. 03, Last sequence update)
 DT 01-MAY-1999 (TREMURel. 10, Last annotation update)
 DE MYELOID ELF-1 LIKE FACTOR.
 GN MEF.
 OS Homo sapiens (Human).
 SO

OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Mammalia:
 OC Eutheria: Primates: Catarrhini: Hominoidea: Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 97050779.
 RA MITSUKAWA Y., SUN X., UCHIDA H., ZHANG J., NIKER S.,
 "Amino acid sequence of the DNA binding site of the
 RT domain of the human c-Jun N-terminal activating protein-1".
 RL Oncogene 13:1721-1728(1996).
 DR EMBL: U32645: AAB55693.1: ".
 DR PFM: PFM0178: Ets: 1.
 DR PROSITE: PS00345: ETS_DOMAIN_1: 1.
 DR PROSITE: PS00346: ETS_DOMAIN_2: 1.
 DR SEQUENCE 663 AA: 70729 MW: D88C987 CRC32.

Query Match 13 7%: Score 245: DB 4: Length 663:
 Best Local Similarity 27 2%: Pred. No. 6: 16-14:
 Matches 86: Conservative 47: Mismatches 103: Indels 80: Gaps 12:

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OY 66 LYPSSMAAKAPGASREPEPEOCF-VYDSOMAPAGSLDVPGLTLE-HS-----119
DB 5 LQPSDLIFEFASNGDDDIHQLEDPVFAVYDVPPPLHLTSLDLVDHNGITTD 64
OY 119 -----LEQNSWNGEYLD-----ITACKLINTADPMDSBNY--OKMLTHER 164
DB 65 GTLCWQDQDILESSFLTDNEMATSHMSTAVLME-----SPEDIDENQIFSTSE 118
OY 165 -----QYRLPPM-----GKAFQELAGKELCANSSEPPORRS 195
DB 119 MLPSDPAVAVTLNLPFASSEPDALNRAGTSDQSGHSLSEKASRESAKTKSKRR- 218
OY 196 PLGGDVLHMHLDLTKSAAMKERTSPGALHWCASISESTDSYDSSGCSQPIHMOFL 235
DB 178 -----LNKTKG--NNSIIP-----VYDSIPIRKSKDOKSGITLMREL 215
OY 286 KELLKLNHSYGRFIRMLKNGKGFIPEDSNQVARIKRNKRNPNMNTDLKSLRSIYTKR 315
DB 216 LALLDQNTCEPKYIKTKOREKGFPLVDKSAVSKLNGKRNKPKDMNTETMGRALRYTOR 275
OY 316 GIIRKPDISORLYTOR 331
DB 276 GILAKVE--GQRLVYOF 290

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Search completed: November 21, 1999, 02:06:12
 Job time: 833 sec

GenCore version 4.5
 Copyright (c) 1993 - 1998 CompuGen Ltd.

OM protein - protein search, using sw model
 Run on: November 21, 1999, 01:52:19 : Search time 16.06 seconds
 (without alignments)
 1283.756 Million cell updates/sec

Title: US-09-126-945-2
 Perfect score: 1785
 Sequence: 1 MGSASPGSLSVSPSHLLPP.....GIIRKPDISORLYTORFHPPI 335

Scoring table: BLOSUM62
 Searched: 201082 seqs, 61543640 residues

Database :
 1: SP:archaea:*
 2: SP:bacteria:*
 3: SP:fungi:*
 4: SP:human:*
 5: SP:invertebrate:*
 6: SP:mammal:*
 7: SP:mbc:*
 8: SP:organelle:*
 9: SP:phage:*
 10: SP:plant:*
 11: SP:protist:*
 12: SP:virus:*
 13: SP:vertebrate:*
 14: SP:unclassified:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1785	100.0	335	4	0953238
2	487.5	27.3	365	5	097145
3	417	23.4	532	5	019695
4	299	16.8	255	4	095175
5	288	16.1	253	11	092826
6	283	15.9	336	6	062804
7	274	15.4	432	13	093425
8	265.5	14.9	435	13	093425
9	256.9	14.4	300	1	017423
10	256.9	14.4	300	1	017423
11	255.5	14.3	440	13	093425
12	252.5	14.1	481	5	017057
13	245.5	14.0	385	4	014319
14	249	13.9	348	4	099718
15	245	13.7	663	4	099607
16	245	13.7	663	4	060435
17	245	13.7	663	4	062803
18	242	13.6	521	4	015724
19	242	13.6	521	4	015724
20	242	13.6	521	4	015724
21	239	13.4	471	13	057565
22	238.5	13.4	371	4	078545
23	235.5	13.2	371	11	035275
24	230.5	12.9	490	13	093425
25	229	12.8	494	13	057566
26	225	12.6	390	13	093425
27	224	12.5	375	13	093425
28	224	12.5	375	13	093425
29	219	12.3	456	4	075645

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30 218.5 12.2 441 5 027378 027378 caenorhabd1
31 218 12.2 428 4 075606 075606 homo sapien
32 213.5 12.0 477 13 09YH6 09YH6 gallus gall
33 212.5 11.9 477 13 09YH6 09YH6 gallus gall
34 209.5 11.7 436 13 09YH6 09YH6 gallus gall
35 203 11.4 538 5 08416 08416 drosophila
36 201.5 11.3 559 5 02665 02665 caenorhabd1
37 201.5 11.3 559 5 02665 02665 caenorhabd1
38 197.5 11.1 268 13 09144 09144 xenopus lae
39 191 10.7 196 4 016203 016203 homo sapien
40 185 10.4 374 4 016199 016199 homo sapien
41 184 10.3 354 5 022355 022355 caenorhabd1
42 181.5 10.2 377 5 022355 022355 caenorhabd1
43 181.5 10.2 377 5 022355 022355 caenorhabd1
44 176 9.9 208 5 018573 018573 homo sapien
45 155.5 8.7 256 13 042415 042415 gallus gall

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ALIGNMENTS

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RESULT 1
ID 095238 PRELIMINARY: PRT: 335 AA.
AC 095238:

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DT 01-MAY-1999 (TREMblrel. 10, Created)
DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMblrel. 10, Last annotation update)
DR EMBL: AF071538: AAC95296.1: "

```

```

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Euharyota; Primates; Catarrhini; Hominoidea; Homo.

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RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;

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RA BOLTJAN, P.; ANGER, E.; ANBARALI, Y.; THAKRONGSAK, U.; DOBE, A.;
RT "Isolation and characterization of a cDNA encoding a prostate
RT epithelium-specific ets transcription factor, PDEF".

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RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF071538: AAC95296.1: "
SQ SEQUENCE 335 AA: 37517 MW: 874ASDE8 CRC32:

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Query Match 100.0% Score 1785; DB 4; Length 335;
Best Local Similarity 100.0%; Pct. No. 4;e-153;
Matches 335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MGSAPQLSSVSPSHLLPPDTVSRGTLEKKAAGAVGLERDMSPSPATPEQGLSARY 60
DB 1 MGSAPQLSSVSPSHLLPPDTVSRGTLEKKAAGAVGLERDMSPSPATPEQGLSARY 60
QY 61 STFDMLYPRDSSAAKAFGASSREPEPEPDCPYDSOAPAGSLDVGGLTLEHSL 120
DB 61 STFDMLYPRDSSAAKAFGASSREPEPEPDCPYDSOAPAGSLDVGGLTLEHSL 120
QY 121 OVSQNVVGVGLKDIETACKLNTITADPMQSPNOVKWLTAEHQYRLPPGKATQELAG 180
DB 121 OVSQNVVGVGLKDIETACKLNTITADPMQSPNOVKWLTAEHQYRLPPGKATQELAG 180
QY 181 KCLCAMEEQFORSPGLGVLAAHLDINKSAANKERTSPGATHTCASTSESWTSEV 240
DB 181 KCLCAMEEQFORSPGLGVLAAHLDINKSAANKERTSPGATHTCASTSESWTSEV 240
QY 241 DSSGSGPIHMOFLKELLKPHSGYGFIRMLKKKGGIFITDSDAVARLIRNP 300
DB 241 DSSGSGPIHMOFLKELLKPHSGYGFIRMLKKKGGIFITDSDAVARLIRNP 300
QY 301 NTDLSNIRQYKKGITIRAPDISORLYOVFVTP 335
DB 301 NTDLSNIRQYKKGITIRAPDISORLYOVFVTP 335

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RESULT 2
ID 097145 PRELIMINARY: PRT: 361 AA.
AC 097145:
DT 01-MAY-1999 (TREMblrel. 10, Created)
DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMblrel. 10, Last annotation update)
DR EMBL: AF071538: AAC95296.1: "
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Euharyota; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PROSTATE;
RA BOLTJAN, P.; ANGER, E.; ANBARALI, Y.; THAKRONGSAK, U.; DOBE, A.;
RT "Isolation and characterization of a cDNA encoding a prostate
RT epithelium-specific ets transcription factor, PDEF".
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF071538: AAC95296.1: "
SQ SEQUENCE 363 AA: 40768 MW: CAB9BDF8 CRC32:

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Query Match 100.0% Score 487.5; DB 5; Length 363;
Best Local Similarity 100.0%; Pct. No. 4;e-153;
Matches 119; Conservative 57; Mismatches 105; Indels 105; Gaps 9;

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QY 1 LSSVSPSHLLPPDTVSRGTLEKKAAGAVGLERDMSPSPATPEQGLSARY 59
DB 1 LSSVSPSHLLPPDTVSRGTLEKKAAGAVGLERDMSPSPATPEQGLSARY 59
QY 23 LAETISGSTLLDLDLIDQO-----ORNGPSPSPSGTGLPSPDMG----- 66
DB 23 LAETISGSTLLDLDLIDQO-----ORNGPSPSPSGTGLPSPDMG----- 66
QY 60 LSTFDMLYPRDSSAAKAFGASSREPEPEPDCPYDSOAPAGSLDVGGLTLEHSL 119
DB 60 LSTFDMLYPRDSSAAKAFGASSREPEPEPDCPYDSOAPAGSLDVGGLTLEHSL 119
QY 66 -----STFDMLYPRDSSAAKAFGASSREPEPEPDCPYDSOAPAGSLDVGGLTLEHSL 119
DB 66 -----STFDMLYPRDSSAAKAFGASSREPEPEPDCPYDSOAPAGSLDVGGLTLEHSL 119
QY 120 EOVSNVGVGLKDIETACKLNTITADPMQSPNOVKWLTAEHQYRLPPGKATQELAG 179
DB 120 EOVSNVGVGLKDIETACKLNTITADPMQSPNOVKWLTAEHQYRLPPGKATQELAG 179
QY 179 KCLCAMEEQFORSPGLGVLAAHLDINKSAANKERTSPGATHTCASTSESWTSEV 240
DB 179 KCLCAMEEQFORSPGLGVLAAHLDINKSAANKERTSPGATHTCASTSESWTSEV 240
QY 241 DSSGSGPIHMOFLKELLKPHSGYGFIRMLKKKGGIFITDSDAVARLIRNP 300
DB 241 DSSGSGPIHMOFLKELLKPHSGYGFIRMLKKKGGIFITDSDAVARLIRNP 300
QY 301 NTDLSNIRQYKKGITIRAPDISORLYOVFVTP 335
DB 301 NTDLSNIRQYKKGITIRAPDISORLYOVFVTP 335
QY 337 IROYKKGITIRAPDISORLYOVFVTP 362
DB 337 IROYKKGITIRAPDISORLYOVFVTP 362

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RA BOFIELD J., BURTON J., CONNELL M., CORSEY T., COOPER J., COULSON A.,
 RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
 RA GARDNER A., GREEN P., HAKINS T., HILLER L., JER M., JOHNSTON L.,
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
 RA LIEBOWITZ J., LLOYD C., MCGRATH A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIKKEN L., ROOPER A., SAUNDERS K., SHONKES R.,
 RA SMITH C., SONNHAUPT D., STANLEY J., STANLEY J., STANLEY J.,
 RA THERRY-MIEG J., THOMAS K., THOMAS K., THOMAS K., THOMAS K.,
 RA WATSON A., WEINSTEIN L., WILKINSON-SPOFFORD J., WOODMAN P.,
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans".
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA HALLSMORTH K.:
 RA Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 RA SEQUENCE FROM N.A.
 RA WATSON R.:
 RA Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U41547; AAA83194.1; -
 DR PFM: PFM0118; Ets: 1.
 SQ SEQUENCE 533 AAs: 60196 MW: 98067676 CRC32:

Query Match 23.4% Score 417; DB 5; Length 532;
 Best Local Similarity 23.4%; Pred. No. 1; 2e-26;
 Matches 127; Conservative 63; Mismatches 116; Indels 218; Gaps 16;

4 ASPGLSPSPHLLPPDYSTRGLEKAAAGVLEER---DMSPPAPPE-----53
 27 ASFGIES-----RESVFGIKVCVAA---RAAPPPEPPPPPTPLFKLSE 72
 53 ---OGLSAYLSIFDKMLT-----PEDS-----MAAKAPASSNEEP---PEE 89
 73 TOFHOLNCAFPPNLEKTKGCKSDSSMNGVGVCHKNLSLP-----EPHGIES 126
 90 PPOCVYDSOAPAGSLD-----VPGGLTE-----EHS---119
 127 TASTPFVKSEFPED-DLFGIDQVANNKPHMDPNIPTPTENRNRSDMDHSTFVK 185
 119 ---LEQVSNNVGEVLDIETACGLNLTADPNDSP 152
 186 NEEIEMLNENFELADNGDLDTQOQIDYRLDLHLHLDISTCKLADNFTLMS 245
 153 SNNOKMLLTHOYRLPMPKAKFOELGKASEEFPQSPAGDYLHMLDWTMSA 212
 246 EHGAWINEMCMOPNLOPPRNC--SITGIDLGSKDFEMLPAGGDTLHMOLOVMTA 303
 213 ---AMNKERTSPGAIHYCASTSEES-----235
 304 FSNVPTVVOSSGTAENNNKSKTMALASTNAGNNOGNNMAAENPNFPGNGYPMNS 363
 235 ---WTDSEYDS 242
 364 MSFPFOGTYLPSNDSOTSGNSODMDDOIDLHNNNSCGFNFNGNYSNPIDA 433
 243 SCSSQ-----PIHLMOFLKELLKPHSYGRTIRMLKNGKIFIKEDSAOVA 288
 424 MKNGBEGDDERATRHOGTVLHMOFRELDOYKTSACNRMVADRGITFRLESSLLA 403
 289 RLMGIRKPRANMAYDLSRSIRYKKGKIRPDSKQSYLYOYVMP 334
 484 RVMGGRKNSOMNTDLRSRLROYKTKGIIOPKRNOLYKFLP 539

RESULT 4
 ID 095175 PRELIMINARY; PRT: 235 AA.
 AC 095175
 KD 095175
 DT 01-MAY-1999 (TITMBLrel: 10, Created)
 DT 01-MAY-1999 (TITMBLrel: 10, Last sequence update)
 DT 01-MAY-1999 (TITMBLrel: 10, Last annotation update)

DE E74-LIKE FACTOR 5.
 GN ELF5.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 CC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA ZHOU J., NG A.Y.N., TYMS M.J., JERMIN L.S., SETH A.K., THOMAS R.S.,
 RA KOALA I.:
 RA "A novel transcription factor, ELF5, belongs to the ELF subfamily of
 RT Ets genes and maps to human chromosome 11p13-15, a region subject to
 RT LOH and rearrangement in human carcinoma cell lines".
 RL Oncogene 17:0-0(1998).
 DR EMBL: AF049703; AAC79755.1; -
 SQ SEQUENCE 255 AAs: 30121 MW: 5179A0D CRC32:

Query Match 16.8% Score 299; DB 4; Length 255;
 Best Local Similarity 33.2%; Pred. No. 2; 3e-19;
 Matches 70; Conservative 42; Mismatches 79; Indels 20; Gaps 4;

135 ETACKLNTITADPNDPMSPSVOKMLMTEHOYKLPMPKAKF---DELAGEELCAMSDEPFA 192
 39 QFACDSYTWVPEPNTKRWEMVLOCCDDYLDTCNICFENRNSIGLOLCSMTDEEFP 98
 193 QNSPLGQVLAHL-----DIKCAAMKERTSPGAIHYCASTSEESMTDSEY 240
 99 EADLGEYLFILNIRTOGVSFPNDASEKATINDYADSN-----CLMTSGIKSDCHS 154
 241 DSSCSQPIHMOFLKELLKPHSYGRTIRMLKNGKIFIKEDSAOVAIRKRRPAA 300
 155 HRTSLSSSHLMFVFDLLSPENCGILEDEDRDGIFFVYKSEALAKMGGKRRNDW 214
 301 NTKLRSIRYKKGKIRPDSKQSYLYOYVMP 331
 215 TELSRLRYTKGILERV-DRLYVTF 243

RESULT 5
 ID 0922K6 PRELIMINARY; PRT: 253 AA.
 AC 0922K6
 KD 01-MAY-1999 (TITMBLrel: 10, Created)
 KD 01-MAY-1999 (TITMBLrel: 10, Last sequence update)
 DT 01-MAY-1999 (TITMBLrel: 10, Last annotation update)
 DE E74-LIKE FACTOR 5.
 GN ELF5.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 CC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA ZHOU J., NG A.Y.N., TYMS M.J., JERMIN L.S., SETH A.K., THOMAS R.S.,
 RA KOALA I.:
 RA "A novel transcription factor, ELF5, belongs to the ELF subfamily of
 RT Ets genes and maps to human chromosome 11p13-15, a region subject to
 RT LOH and rearrangement in human carcinoma cell lines".
 RL Oncogene 17:0-0(1998).
 DR EMBL: AF049702; AAC79754.1; -
 SQ SEQUENCE 255 AAs: 29971 MW: 7892A08A CRC32:

Query Match 16.1% Score 288; DB 11; Length 253;
 Best Local Similarity 33.9%; Pred. No. 2; 2e-18;
 Matches 68; Conservative 43; Mismatches 82; Indels 14; Gaps 5;

135 ETACKLNTITADPNDPMSPSVOKMLMTEHOYKLPMPKAKF---DELAGEELCAMSDEPFA 192
 39 QFACDSYTWVPEPNTKRWEMVLOCCDDYLDTCNICFENRNSIGLOLCSMTDEEFP 98
 193 QNSPLGQVLAHL-----DIKCAAMKERTSPGAIHYCASTSEESMTDSEY 240
 99 EADLGEYLFILNIRTOGVSFPNDASEKATINDYADSN-----CLMTSGIKSDCHS 156


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Qy 183 LCANSEDFORRSPGLGDVLAH-----AHLD-----INSAAMKERTSPGAIHCASIS 232
Db 128 LBYSLRNP-EHLSNGDVAHDDSTSSDEPOKNSPRTATYR-KRRRARRSPRTY 184
Qy 233 ESWTDEVSOCSCOPILHMOFLKELLKPHSGFIMLANKGIFKIEDSNOVAILNG 292
Db 185 PELAKKSKGEGNTIYMEFLALLODKNCTPKXIMGSENGIFLVDKAAVSKLNG 244
Qy 293 IKRRPAMNYDKLSISROYKKGKIJRRPDSORLATO 331
Db 245 KHKRKNMYETMGALRYTGRIACKE-CGRVLTOF 282

RESULT 9
Qy 05723 PRELIMINARY: PRT: 581 AA.
ID 015723:
AC 01-NOV-1996 (TReMBrel. 01, Created)
DT 01-NOV-1996 (TReMBrel. 01, Last sequence update)
DE 01-MAY-1999 (TReMBrel. 10, Last annotation update)
DE ETS TRANSCRIPTION FACTOR.
GN NERF-2.
OS Homo sapiens (Human)
OC Eukaryota; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN, FETAL LIVER, FETAL BRAIN:
RX MEDLINE: 96347578.
RA OELTEN P., ANBARALI Y., BOLTAJ J., BEST J., KUNSC C.,
LIBERMAN T.A.;
RT Characterization of NERF, a novel transcription factor related to
RT the Ets family of transcription factors.
RL Mol. Cell Biol. 16:5091-5106(1996).
DR PFAM: PF00178; Ets; 1.
DR PROSITE: PS00345; ETS_DOMAIN; 1.
DR PROSITE: PS00346; ETS_DOMAIN; 2; 1.
SQ SEQUENCE 581 AA: 62711 MW: 2EE2228A CRC32:

Query Match 14.4% Score 257, DB 4: Length 581:
Best Local Similarity 25.5%, Pred. No. 4, 28-15,
Matches 77; Conservative 50; Mismatches 97; Indels 78; Gaps 9:

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AC 070273:
DT 01-AUG-1998 (TReMBrel. 07, Created)
DT 01-AUG-1998 (TReMBrel. 07, Last sequence update)
DE 01-MAY-1999 (TReMBrel. 10, Last annotation update)
DE ETS HOMOLOGOUS FACTOR (EHF) (EHF).
OS Eus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PTUITARY.
RX MEDLINE: 98262938.
RA BODENKE R.A., KLEINMANOV L.A., SUN L.Y., BURTON F.H.;
RT Characterization of the human Ets-related transcription factor/
RT transcription factor/oncoprotein gene family.
RL Biochem. Biophys. Res. Commun. 246:176-181(1998).
DR EMBL: AF035527; AAC0119.1; -.
DR MGI: MGI1270840; EHF.
DR PFAM: PF00178; Ets; 1.
SQ SEQUENCE 300 AA: 34903 MW: 383FE286 CRC32:

Query Match 14.4% Score 256.5, DB 11: Length 300:
Best Local Similarity 28.0%, Pred. No. 1, 9e-15,
Matches 69; Conservative 47; Mismatches 65; Indels 65; Gaps 9:

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Qy 147 PWDSSNYOQWMLTTEHOYRLPMEKAFQF-LAGEKLCANSEDFORRSPGLGDVLAH 204
Db 47 POYTKYQWEMTGLDTRDOLDASCPFOEFGISGELCSMSQETFRPAAGSAGQLYS 106
Qy 205 H-----DIKSA--ANKERTSPGAIHCASISSEST-----DEVD----- 242
Db 107 NQHLKMGQSSDLDQSHNYVYKEDQPSIN--TKENYLYQDSYSGSTYDLDS 163
Qy 242 -SSGSC-----PI-----HMOFLKELLKPHSV 265
Db 164 KTFEKAQISWTSSHLPAESPDKKEDPHVSTKRNHPGTHLMEFIDILLSPKN 223
Qy 266 GFIRLNLKKEGIFKIEDSNOVAILNGIKRRPAMNYDKLSISROYKKGKIJRRPDS 325
Db 224 POLIKRMESSGIFRFLKLSAIVQDNGKKNNSMTKLSHAKATTKRLEIRVGR 282
Qy 326 RLYYKF 331
Db 283 RLYYKF 288

RESULT 11
QyHUS PRELIMINARY: PRT: 440 AA.
ID 09YHUS:
AC 09YHUS:1999 (TReMBrel. 10, Created)
DT 01-MAY-1999 (TReMBrel. 10, Last sequence update)
DE TRANSCRIPTION FACTOR Egr1.
DE Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Actinopterygii; Neopterygii;
OC Teleostei; Euteleostei; Acanthopterygii; Perciformes;
OC Tetraodontiformes; Tetraodontidae; Tetraodontidae; Fugu.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 98252118.
RA VILLARD L., TASSONE F., CRNOSGAC-JURCEVIC T., CLANCY K.,
RA GARDNER K.;
RT Analysis of pufferfish homologues of the At-rich human App gene.
RT Gene 210:17-24(1998).
RN [2]
RP TASSONE F., VILLARD L., CLANCY K., GARDNER K.;
RT The transcription factor Egr1 is the pufferfish homologue of the
RT cyathionine beta-synthetase genes from Fugu rubripes.

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RL Gene 226:211-223(1999).
 DR EMBL: AF090120: AD13395.1;
 SQ SEQUENCE 440 AA: 49595 MW: 0E3E74F6 CRC32:
 Query Match 14 38: Score 255.5; DB 13; Length 440;
 Best Local Similarity 24.68; Pred. No. 6-15;
 Matches 78; Conservative 50; Mismatches 110; Indels 79; Gaps 8;
 QY 60 LSYEDMLYEDSSMAKAPASSREPEPEECQPIYISO--APAGSGLDLPAGGLTEH 117
 Db 107 LNIETLKEVEVEVVIDPPAGGEGALVEQGLDINVERGUSLSDAEQYTRMAALLEG 166
 QY 118 SLEVOSSMNGVEVLADITKCLINTADPMQSPNSYOKMLTLETOYRLPRGKAFOF 177
 Db 167 RKEOVR-----LGIPYPLASADQYIVMAVVMKEINDEMEISIH 209
 QY 178 LAGELCALMSEDFRORSPLAGSDVLAHMLDITMSAMMKERTSGAHYCASTSESWTD 237
 Db 210 IFGRDLCSFSQEFQKVP--NEGILMSHETELR-----YLASDQSCGD 254
 QY 238 SEV-----DSCSGO-----PIHMOET 255
 Db 255 AVITIDPOVITPTQVNTPTAKVLKQSGPRAPRISEBRSQGNRNNQNGIOWEL 314
 QY 256 KELLKPHSYGRFIRMLKNGKIFKIEDSAQVARLNGIRPNAPYADKRSIRQYKK 315
 Db 315 LELLTDKN--RCCIYRGEGEGRILNOPELQAKMGQRNNPTMYEKLSRALTYYID 372
 QY 316 GIKRKDPSISORLYOYF 332
 Db 373 DWISKVO-GKRFVNEFV 388
 RESULT 12
 QY 017057 PRELIMINARY: PRT: 481 AA.
 AC 017057;
 DT 01-JAN-1998 (TREMblrel. 05, Created)
 DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
 DT 01-MAY-1999 (TREMblrel. 10, Last annotation update)
 DE C24AL.2 PROTEIN.
 GN C24AL.2
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabdittia; Rhabdittida;
 RN [1]
 RA Rhabdittia; Rhabdittidae; Rhabdittidae; Pelodidae; Caenorhabdittia.
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE: 94150718.
 RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
 RA BONFIELD J., BURTON J., CONNELL M., COOPER T., COOPER J., COULSON A.,
 RA CRATON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
 RA JONES A., GREEN P., HARKINS T., HILLIER L., JIER M., JOHNSTON L.,
 RA LIGHTNING L., KENNEDY R., KITCHEN L., LAISTER N., LATREILLE P.,
 RA PARSONS J., PERCY C., RIFKEN L., ROOPDRAKSHANDAS C., THOMKSEN R.,
 RA SHALDON N., SMITH A., SONNHAMMER E., STADEN R., SUTTON J.,
 RA THIRRY-WING J., THOMAS K., VADDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPOUT J., WOLLMAN P.,
 RT 2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RL Mature 368,32-38(1994).
 RL 13
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA CONNELL M.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA WATERSTON R.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF024491: AAB7011.1;
 DR PRAN: PF00178: ETS.DOMAIN.1.1;
 DR PROSITE: PS00345; ETS.DOMAIN.1.1;
 DR PROSITE: PS00346; ETS.DOMAIN.2.1;
 SQ SEQUENCE 481 AA: 53773 MW: 575FAEBB CRC32:
 Query Match 14 18: Score 252.5; DB 5; Length 481;
 Best Local Similarity 51.18; Pred. No. 8-3e15;
 Matches 45; Conservative 20; Mismatches 22; Indels 1; Gaps 1;
 QY 246 GQPHLMQFKEILLKPHSYGRFIRMLKNGKIFKIEDSAQVARLNGIRPNAPYADK 305
 Db 335 GQVYLMSEFLRLDQYSPKFKIMQKIFKIEDSKAVSRILMGHNRPNQNYETH 394
 QY 306 SRSIRQYKKGITRIPDISORLYOYFV 333
 Db 395 GRLRYTQGLQAND--GQMLYRHYH 421
 RESULT 13
 QY 014319 PRELIMINARY: PRT: 385 AA.
 AC 014319;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-MAY-1999 (TREMblrel. 10, Last annotation update)
 DE FLI-1.
 GN FLI-1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 RN [1]
 RA Rhabdittia; Primates; Catarrhini; Hominoidea; Homo.
 RP SEQUENCE FROM N.A.
 RC TISSUE-BLOOD.
 RX MEDLINE: 93176799.
 RA HOKMAS R., MAY M., DENNY C., BASKIND W., MOORE J., MAKI R.A., BECK E.,
 RA KLEMS M.J.;
 RT Human FLI-1 localizes to chromosome 11Q24 and has an aberrant
 RT transcript in neuroblastoma.
 RL 13
 DR EMBL: M93257: AAL58450.1;172:135-158(1993).
 DR PRAN: PF00178; ETS.1.1;
 DR PROSITE: PS00345; ETS.DOMAIN.1.1;
 DR PROSITE: PS00346; ETS.DOMAIN.2.1;
 SQ SEQUENCE 385 AA: 43437 MW: 0820C243 CRC32:
 Query Match 14 08: Score 249.5; DB 4; Length 385;
 Best Local Similarity 28.08; Pred. No. 1-2e-14;
 Matches 87; Conservative 40; Mismatches 107; Indels 77; Gaps 12;
 QY 79 GASSEPEPEPEPECCVIDSOAPNCSLDYAPGSGT-----LEHSLEQSSMNGVEY 130
 Db 3 GGLAGEBARSPVCSV-----SCKCKALVGGSHPNPNVNSYDEKNPPPPMTNE- 56
 QY 131 LNDIEFCKLINTADPMQSPNSYOKMLTLETOYRLPRGKA-FOELAKRELCAMSEF 189
 Db 56 -----KRIYVPAKLTALVQCHORHMLKLEKLSLMEIDTSFQNDKRELCAMKE 107
 QY 190 QFORSPL--GSDVLAHMLDITMSAMMKERTSGAHYCASTSESWTD 237
 Db 108 DFLRATLVNTEVILSHSLYRESLAVNTSHTDQSSRLSKEDSYSDVRGAKNN 167
 QY 218 RTSP-----GAHYCASTSEF-----SMTDEYDSCSGQPIHLMQFLKELL 260
 Db 168 MNSGLNKSPPDLGAGQTIKRTDNRQDPDYQIIGPSSIRLANSQGO-IQLMPLFLF-L 225
 QY 261 KPHSYGRFIRMLKNGKIFKIEDSAQVARLNGIRPNAPYADKRSIRQYKGIIR 320
 Db 226 SDAVASCIIT--EGTNGEFTANDPQVLAHNRQCHSKRTNNVADKLSRLATITDKNITN 284
 QY 321 PDISORLYOYF 331

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Db      285 VH-GKRYAKF 294
          :| |
RESULT   14
099718 PRELIMINARY: PRT: 348 AA.
AD 099718
DT 01-MAY-1997 (TREMblrel_03 Created)
DT 01-MAY-1997 (TREMblrel_03 Last sequence update)
DT 01-NOV-1998 (TREMblrel_08 Last annotation update)
DE EPIHELIAL-SPECIFIC TRANSCRIPTION FACTOR ESE-1A.
GN ESE-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN [1] SOURCE FROM N.A.
RC TISSUE=ADULT LIVER, PANCREATIC CARCINOMA.
RX MEDLINE: 97378019
RA BOLTJAN J., KUNSH C., BUNCGER K., LISERMAN T.A.,
RT Isolation and characterization of a novel epithelium-specific
transcription factor, ESE-1, a member of the ets family.*
RL EMBL: U73844; AAB55824.1.;
DR PRAM; PF00178; Ect: 1; 39357 MW; 274B3FA2 CRC32;
SEQUENCE 348 AA: 39357 MW; 274B3FA2 CRC32;

Query Match      13.9% Score 249; DB 4; Length 348;
Best Local Similarity 24.4%; Pred. No.1,1e-14;
Matches 89; Conservative 53; Mismatches 95; Indels 128; Gaps
DB      7 ISNLSITSNMSSSDSLATYPA-----KTSNDLV---LTL 44
OY      55 LSATFYSYFDMLYPEDSSMAAPQASSHESPEPEECVCYTDSQAPAGSJDLYPGGLTL 114
        |||||
OY      115 E--EHSLEOVG-SMYGVGVKAKIETACGLKLNTVDPMDSPPSVOKYLWL--TEHOYRLP 169
        |||||
DB      45 SNPMSIEGTETKSMVLGE-----QPDMSKTOYLDWISYOVEKNKYDAS 88
OY      170 PKCAFOELDLACKELCMSEBOFR-QRSPLGSVDYLAHL-CINKSA-----AMN----- 216
DB      89 ALDSRDMDGATLCACMLELRLVPEPL-ODQLAHQDRLTSSSDSELSTWIELLEOG 147
OY      216 ---KERSPGAHKCSSESESPD-----SEPD----- 202
DB      148 ICFEALDPCEFGSGPAPDELDDVSTAGTCGASRSHSSSDSGSDVDLDPDGKLFPSD 207
OY      242 --SSCS-----GCP-----ILHMDFKELLNLPHSYG 266
DB      208 GFROCKGDPKHGKRGRERRRKILEYWDCLGGKKSKARPRGHILAEFLRIHLHELMNE 267
OY      267 RTIRALMEKGITRIEDSAOVAVALMGIRKRRPAMPTDKLSIRIOYKGIKIKRPDISOR 326
DB      268 GLMKREMHIEGYRTFBEAVNQIDHQKKKSMTTELBSMRKIYKKEELLEND--GR 326
OY      327 LVYGF 331
        |||||
DB      327 LVYKF 331
        |||||

RESULT 15
099607 PRELIMINARY: PRT: 663 AA.
AD 099607
DT 01-MAY-1997 (TREMblrel_03 Created)
DT 01-MAY-1997 (TREMblrel_03 Last sequence update)
DT 01-MAY-1999 (TREMblrel_10 Last annotation update)
DE MYELOID ELF-1 LIKE FACTOR.
GN ELF-1.
OS Homo sapiens (Human).

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OC      Eutheria: Metaceae: Chiroptera: Chiroptera: Vespertilionidae: Mammalia:
OC      Eutheria: Primates: Catarrhini: Hominoidea: Homo.
RN      [1]
RP      SEQUENCE FROM N.A.
RA      MEDLINE: 9705079.
RX      ATLANTIC, J. SUN X., UCHIDA H., ZHANG J., NIMER S.;
RA      "A novel human placental chondroitinase A-like DNA binding
RT      domain that facilitates chondroitin sulfate proteoglycan
RT      degradation by binding to the chondroitin sulfate activating properties."
RL      Oncogene 13:11721-1728(1995).
DR      PRLM: U32645: A853563.1.
DR      PRLM: P00178: Eta. 1.
DR      PROSITE: PS00345: ETS_DOMAIN.1.
DR      PROSITE: PS00346: ETS_DOMAIN.2.
SQ      SEQUENCE 663 AA: 70729 MW: D88CC987 CRC32:

Query Match      13.78: Score 245; DB 4: Length 663.
Best Local Similarity 21.78; Pident. No. 6; Id 145.
Matches 86: Conservative 47; Pident. 103; Indels 80; Gaps 12.

Oy      66 TTPEDSSAAKAKGASNSHEEPEDQCYTSSAPGASGLVYGGTLTEFHS-----119
Db      5 LQPSDLTFEPASNGDDDIHQLEDPSPVAVYEQYPPDLTLTSGCLDQVHNGITTD 64

Oy      119 -----LEQVDSWVYGEVLAD-----IFETACKLLNITAPDMSPEPNV--QKMLMTER 164
Db      65 GTLMTQDQDILLESFLLDNDENATSHMTAEVLAHMC-----SPQDILDEQDITSTSE 118

Oy      165 -----QYRLPPM-----GKAQDLAKGELCANKSEDFQNR 195
Db      119 MLPDSDPAANTLPNTLPFASPDALNRAGDTSDQDSHSLSEKASREDSAGKSKNR 178

Oy      195 PLGGDVLVAHLDITWSSAAANKKERTSPALHYTCASSTSESTQSEVSDSGSOPPLHMQPFL 255
Db      198 -----TRKNG--NISTSP-----YDSDSLPRKSKDQKSTLYLMEFL 215

Oy      235 KELLNPHSYGRFIRMLNKKSGIFPIEDSAAVVAWLGIKRRNPANMYDRLSRISROYKK 315
Db      216 LALLDNNCTCRKYIKNTQRFKQGLFELVDKSKANSGKNNKPNNDIETHEMRALRYIQR 275

Oy      316 GIIKRPDGLQALYQ 331
Db      275 GILAKVE--QGLRYQGR 290

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